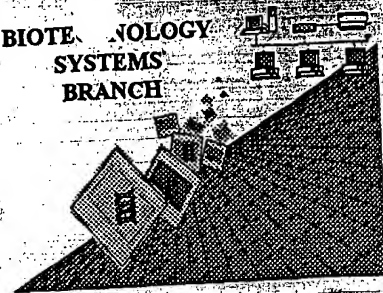


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/325,602

Source: 1653

Date Processed by STIC: 7/28/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Input Set : A:\ES.txt
Output Set: N:\CRF3\07282000\I325602.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Galdes, Alphonse
8 Mahanthappa, Nagesh
9 Engber, Thomas
11 (ii) TITLE OF INVENTION: Methods and Compositions for Treating Disorders
12 Involving Excitotoxicity
14 (iii) NUMBER OF SEQUENCES: 22
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Foley, Hoag & Eliot LLP
18 (B) STREET: One Post Office Square
19 (C) CITY: Boston
20 (D) STATE: MA
21 (E) COUNTRY: USA
22 (F) ZIP: 02109
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: ASCII (text)
30 (vi) CURRENT APPLICATION DATA:
C--> 31 (A) APPLICATION NUMBER: US/09/325,602
C--> 32 (B) FILING DATE: 03-Jun-1999
33 (C) CLASSIFICATION:
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Vincent, Matthew P.
37 (B) REGISTRATION NUMBER: 36,709
38 (C) REFERENCE/DOCKET NUMBER: BIV-069.02
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: (617) 832-1000
42 (B) TELEFAX: (617) 832-7000

ERRORED SEQUENCES

951 (2) INFORMATION FOR SEQ ID NO: 8:
953 (i) SEQUENCE CHARACTERISTICS:
954 (A) LENGTH: 1191 base pairs
955 (B) TYPE: nucleic acid
956 (C) STRANDEDNESS: both
957 (D) TOPOLOGY: linear
959 (ii) MOLECULE TYPE: cDNA
962 (ix) FEATURE:
963 (A) NAME/KEY: CDS
964 (B) LOCATION: 1..1191
967 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
969 ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG

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Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/325,602

DATE: 07/28/2000
 TIME: 09:30:19

Input Set : A:\ES.txt
 Output Set: N:\CRF3\07282000\I325602.raw

970	Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu	
971	1				5				10				15				
973	GC	CTG	CCA	GCC	CAG	AGC	TGC	GGG	CCG	GGC	CGG	GGG	CCG	GTT	GGC	CGG	96
974	Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg	
975				20				25					30				
977	CGC	CGC	TAT	GCG	CGC	AAG	CAG	CTC	GTG	CCG	CTA	CTC	TAC	AAG	CAA	TTT	144
978	Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	
979			35				40				45						
981	GTG	CCC	GGC	GTG	CCA	GAG	CGG	ACC	CTG	GGC	GCC	AGT	GGG	CCA	GCG	GAG	192
982	Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
983		50				55					60						
985	GGG	AGG	GTG	GCA	AGG	GGC	TCC	GAG	CGC	TTC	CGG	GAC	CTC	GTG	CCC	AAC	240
986	Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
987	65			70				75				80					
989	TAC	AAC	CCC	GAC	ATC	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGT	GGA	GCC	GAC	288
990	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
991				85				90				95					
993	CGC	CTG	ATG	ACC	GAG	CGT	TGC	AAG	GAG	AGG	GTG	AAC	GCT	TTG	GCC	ATT	336
994	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
995			100					105				110					
997	GCC	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTG	CGC	CTA	CGA	GTG	ACT	GAG	GGC	384
998	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
999		115				120					125						
1001	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCT	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
1002	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
1003		130				135					140						
1005	CGT	GCT	TTG	GAC	ATC	ACT	ACG	TCT	GAC	CGC	GAC	CGC	AAC	AAG	TAT	GGG	480
1006	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
1007	145				150					155			160				
1009	TTG	CTG	GCG	CGC	CTC	GCA	GTG	GAA	GCC	GGC	TTC	GAC	TGG	GTC	TAC	TAC	528
1010	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
1011				165				170				175					
1013	GAG	TCC	CGC	AAC	CAC	GTC	CAC	GTG	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
1014	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
1015			180					185				190					
1017	GCG	GTC	CGG	GCG	GGC	GGC	TGC	TTT	CCG	GGA	AAT	GCA	ACT	GTG	CGC	CTG	624
1018	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
1019		195				200					205						
1021	TGG	AGC	GGC	GAG	CGG	AAA	GGG	CTG	CGG	GAA	CTG	CAC	CGC	GGA	GAC	TGG	672
1022	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
1023		210				215					220						
1025	GTT	TTG	GCG	GCC	GAT	GCG	TCA	GGC	CGG	GTG	GTG	CCC	ACG	CCG	GTG	CTG	720
1026	Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
1027	225				230						235				240		
1029	CTC	TTC	CTG	GAC	CGG	GAC	TTG	CAG	CGC	CGG	GCT	TCA	TTT	GTG	GCT	GTG	768
1030	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
1031				245				250				255					
1033	GAG	ACC	GAG	TGG	CCT	CCA	CGC	AAA	CTG	TTG	CTC	ACG	CCC	TGG	CAC	CTG	816
1034	Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/325,602
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Input Set : A:\ES.txt
 Output Set: N:\CRF3\07282000\I325602.raw

1035 260 265 270
 1037 GTG TTT GCC GCT CGA GGG CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG 864
 1038 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 1039 275 280 285
 1041 GTG TTC GCG CGC CGG CTA CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC 912
 1042 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 1043 290 295 300
 1045 GGG GAT GCG CTT CGG CCA GCG GCG GTG GCC CGT GTG GCG CGG GAG GAA 960
 1046 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 1047 305 310 315 320
 1049 GCC GTG GGC GTG TTC GCG CCG CTC ACC GCG CAC GGG ACG CTG CTG GTG 1008
 1050 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 1051 325 330 335
 1053 AAC GAT GTC CTG GCC TCT TGC TAC GCG GTT CTG GAG AGT CAC CAG TGG 1056
 1054 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 1055 340 345 350
 1057 GCG CAC CGC GCT TTT GCC CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG 1104
 1058 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 1059 355 360 365
 1061 CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT 1152
 1062 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 1063 370 375 380
 E--> 1065 CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GCG TG 1191 1190
 1066 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 OK 1067 385 390 395
 2333 (2) INFORMATION FOR SEQ ID NO: 22:
 2335 (i) SEQUENCE CHARACTERISTICS:
 2336 (A) LENGTH: 167 amino acids
 2337 (B) TYPE: amino acid
 2338 (D) TOPOLOGY: linear
 2340 (ii) MOLECULE TYPE: peptide
 2342 (v) FRAGMENT TYPE: internal
 2346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 W--> 2348 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Xaa Xaa Xaa Pro Lys
 2349 1 5 10 15
 W--> 2351 Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 2352 20 25 30
 W--> 2354 Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Arg Xaa
 2355 35 40 45
 W--> 2357 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 2358 50 55 60
 W--> 2360 Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 2361 65 70 75 80
 W--> 2363 Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 2364 85 90 95
 W--> 2366 Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 2367 100 105 110
 W--> 2369 His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 2370 115 120 125

(next page)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/325,602

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Input Set : A:\ES.txt

Output Set: N:\CRF3\07282000\I325602.raw

W--> 2372	Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala	
2373	130	135
W--> 2375	Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa	140
2376	145	150
W--> 2378	His Xaa Ser Val Lys Xaa Xaa	155
2379		160
E--> 2383	165	

87
delete at end of file

VERIFICATION SUMMARY

DATE: 07/28/2000

PATENT APPLICATION: US/09/325,602

TIME: 09:30:20

Input Set : A:\ES.txt

Output Set: N:\CRF3\07282000\I325602.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1065 M:254 E: No. of Bases conflict, Input:1191 Counted:1190 SEQ:8
L:1067 M:204 E: No. of Bases differ, LENGTH:Input:1191 Counted:1190 SEQ:8
L:1762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2383 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22